

IN THE CLAIMS:

1. (Currently amended) A method of detecting a difference of one or more nucleotides between a nucleic acid molecule to be tested and a reference nucleic acid molecule wherein the location of said one or more nucleotides that are different between the nucleic acid molecule to be tested and the reference nucleic acid molecule is unknown, said method comprising subjecting the test nucleic acid molecule to single-base-specific cleavage to generate oligonucleotide fragments, separating the resulting oligonucleotide fragments based on mass by MALDI-TOF MS to produce a fingerprint of the oligonucleotide fragments comprising one or more peaks wherein a peak represents the mass of each fragment and identifying an altered peak relative to said reference nucleic acid molecule subjected to the same procedure wherein the presence of an altered peak is indicative of a difference of one or more nucleotides in said tested nucleic acid molecule relative to said reference nucleic acid molecule.
2. (Original) A method according to claim 1 wherein the nucleic acid molecule to be tested is amplified by a polymerase chain reaction (PCR) prior to base specific cleavage.
3. (Previously Presented) A method according to claim 1 wherein the base specific cleavage results in oligonucleotide fragments of from about 2 bases to about 1000 bases.
4. (Original) A method according to claim 3 wherein the base specific cleavage results in oligonucleotide fragments of from about 3 bases to about 500 bases.
5. (Original) A method according to claim 4 wherein the base specific cleavage results in oligonucleotide fragments of from about 4 bases to about 100 bases.
6. (Previously presented) A method according to claim 1 wherein the base specific cleavage is uracil specific cleavage.
7. (Original) A method according to claim 6 wherein the uracil specific cleavage is mediated by uracil-N-glycosylase.

8. (Previously presented) A method according to claim 1 further comprising subjecting the oligonucleotide fragments to further separation to generate a spectrum from decay dependent on the nucleotide sequence of the oligonucleotide.

9. (Previously presented) A method according to claim 8 wherein the further separation of the oligonucleotide fragments is by post source decay (PSD).

10-23. (Cancelled)

24. (Currently amended) A method for identifying or locating a mutation in one or more bases in a target nucleic acid molecule ~~of at least 250 bp in length~~ wherein the location of said mutation within the target nucleic acid molecule is unknown, comprising subjecting the target nucleic acid molecule to single-base-specific cleavage to generate oligonucleotide fragments, separating the resulting oligonucleotide fragments based on mass by MALDI-TOF MS to produce a fingerprint of the oligonucleotide fragments comprising one or more peaks wherein a peak represents the mass of each fragment, and identifying an altered peak relative to said reference nucleic acid molecule subjected to the same procedure, wherein the presence of an altered peak is indicative of a mutation in one or more bases in said target nucleic acid molecule relative to said reference nucleic acid molecule.

25. (Original) A method according to claim 24 wherein the nucleic acid molecule to be tested is amplified by a polymerase chain reaction (PCR) prior to base specific cleavage.

26. (Previously presented) A method according to claim 24 wherein the base specific cleavage results in oligonucleotide fragments of from about 2 bases to about 1000 bases.

27. (Original) A method according to claim 26 wherein the base specific cleavage results in oligonucleotide fragments of from about 3 bases to about 500 bases.

28. (Original) A method according to claim 27 wherein the base specific cleavage results in oligonucleotide fragments from about 4 bases to about 100 bases.

29. (Previously presented) A method according to claim 24 wherein the base specific cleavage is uracil specific cleavage.

30. (Original) A method according to claim 29 wherein the uracil specific cleavage is mediated by uracil-N-glycosylase.

31. (Previously presented) A method according to claim 24 further comprising subjecting the oligonucleotide fragments to further separation to generate a spectrum from decay dependent on the nucleotide sequence of the oligonucleotide.

32. (Original) A method according to claim 31 wherein the further separation of fragmentation products is by post source decay (PSD).

33. (Currently amended) A method of detecting a difference of one or more nucleotides between a nucleic acid molecule to be tested and a reference nucleic acid molecule wherein the location of said one or more nucleotides that are different between the nucleic acid molecule to be tested and the reference nucleic acid molecule is unknown, said method comprising subjecting the test molecule to single-base-specific cleavage to generate oligonucleotide fragments, separating the resulting oligonucleotide fragments based on mass by MALDI-TOF MS to produce a fingerprint of the oligonucleotide fragments comprising one or more peaks wherein a peak represents the mass of each fragment, and identifying an altered peak relative to said reference nucleic acid molecule subjected to the same procedure, wherein the presence of an altered peak is indicative of said difference of one or more nucleotides in said tested nucleic acid molecule relative to said reference nucleic acid molecule, and wherein the difference does not result in a change of a cleavage site.

34. (Canceled)

35. (Currently amended) A method for identifying or locating a mutation in one or more bases in a target nucleic acid molecule wherein the mutation does not result in a change of a cleavage site by a restriction enzyme and wherein the location of said mutation within the target nucleic acid molecule is unknown, comprising subjecting the target nucleic acid molecule to single-base-specific cleavage to generate oligonucleotide fragments, separating the resulting oligonucleotide fragments based on mass by MALDI-TOF MS to produce a fingerprint of the oligonucleotide fragments comprising one or more peaks wherein a peak represents the mass of each fragment, and identifying an altered peak relative to a reference nucleic acid molecule subjected to the same procedure, wherein the presence of an altered peak is indicative of a mutation in one or more bases in said target nucleic acid molecule relative to said reference nucleic acid molecule, and wherein the difference does not result in a change of a cleavage site by a restriction enzyme.